

ENTERED

See p. 6



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,729

DATE: 08/13/2002

TIME: 15:41:44

Input Set : A:\53-99a.app

Output Set: N:\CRF3\08132002\J030729.raw

3 <110> APPLICANT: Hill, Ronald J.
 4 Hannan, Garry N.
 6 <120> TITLE OF INVENTION: GENETIC SEQUENCES ENCODING STEROID AND JUVENILE HORMONE
 7 RECEPTOR POLYPEPTIDES AND INSECTICIDAL MODALITIES
 8 THEREFOR
 10 <130> FILE REFERENCE: 53-99A
 12 <140> CURRENT APPLICATION NUMBER: 10/030,729
 13 <141> CURRENT FILING DATE: 2002-01-02
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00799
 16 <151> PRIOR FILING DATE: 2000-06-30
 18 <150> PRIOR APPLICATION NUMBER: US 09/346,470
 19 <151> PRIOR FILING DATE: 1999-07-01
 21 <160> NUMBER OF SEQ ID NOS: 42
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2274
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Lucilia cuprina
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(2271)
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 37 1 5 10 15
 39 atg tta gaa gaa tcc tcc tca gaa gta acc tcc tcc tca aat ggt ctg 96
 40 Met Leu Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Asn Gly Leu
 41 20 25 30
 43 gtc ttg tca tcg gat ata aat atg tca cct tcc tcg ttg gat tca ccc 144
 44 Val Leu Ser Ser Asp Ile Asn Met Ser Pro Ser Ser Leu Asp Ser Pro
 45 35 40 45
 47 gtt tat ggc gat cag gaa atg tgg ctg tgt aac gat tca gct tca tat 192
 48 Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr
 49 50 55 60
 51 aat aac agt cat cag cat agt gtt ata act tcg ctg cag ggc tgc acc 240
 52 Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr
 53 65 70 75 80
 55 tca tca ttg ccg gcc caa aca acc att ata cct ctg tca gct tta ccc 288
 56 Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
 57 85 90 95
 59 aat tcc aat aat gcc tcc ctg aat aat caa aat caa aat tat caa aat 336
 60 Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn
 61 100 105 110

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64 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val
65      115      120      125
67 gga gga ggt gga ggt ggt ggt ggt gta ccc ggt atg act tca ctc aat 432
68 Gly Gly Gly Gly Gly Gly Gly Gly Val Pro Gly Met Thr Ser Leu Asn
69      130      135      140
71 ggt ctg ggt ggt ggt ggt ggc agt caa gtg aat aat cac aat cac agc 480
72 Gly Leu Gly Gly Gly Gly Gly Gly Ser Gln Val Asn Asn His Asn His Ser
73 145      150      155      160
75 cac aat cat tta cac cac aac agc aac agt aat cac agt aat agc agt 528
76 His Asn His Leu His His Asn Ser Asn Ser Asn His Ser Asn Ser Ser
77      165      170      175
79 tcc cac cac aca aat ggc cac atg ggt att ggc ggc ggt ggt ggt ggc 576
80 Ser His His Thr Asn Gly His Met Gly Ile Gly Gly Gly Gly Gly Gly
81      180      185      190
83 tta tcg gtc aat att aat ggt ccc aat atc gtt agc aat gcc caa cag 624
84 Leu Ser Val Asn Ile Asn Gly Pro Asn Ile Val Ser Asn Ala Gln Gln
85      195      200      205
87 tta aac tcg tta cag gcc tca caa aat ggc caa gtt att cat gcc aat 672
88 Leu Asn Ser Leu Gln Ala Ser Gln Asn Gly Gln Val Ile His Ala Asn
89      210      215      220
91 att ggc att cac agt atc atc agt aat gga tta aat cat cat cac cat 720
92 Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His His
93 225      230      235      240
95 cat cat atg aat aac agt agt atg atg cat cat aca ccc aga tct gaa 768
96 His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu
97      245      250      255
99 tca gct aat tcc ata tca tca ggt cgt gat gat ctt tca ccc tcg agc 816
100 Ser Ala Asn Ser Ile Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser
101      260      265      270
103 agt ctt aat ggc ttc tca aca agc gat gct agt gat gtt aag aaa atc 864
104 Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile
105      275      280      285
107 aaa aaa ggt cct gcg ccc cgt tta caa gag gaa ctg tgt ctg gtg tgt 912
108 Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys
109      290      295      300
111 ggt gat cgg gcg tcc ggt tat cat tat aac gca ctc acc tgt gaa ggc 960
112 Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly
113 305      310      315      320
115 tgt aag ggg ttc ttt cga cgg agt gtt acc aaa aat gcg gtg tat tgt 1008
116 Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Cys
117      325      330      335
119 tgt aaa ttt ggt cat gcc tgc gaa atg gac atg tat atg cga cgt aaa 1056
120 Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys
121      340      345      350
123 tgt cag gaa tgt agg ctg aaa aaa tgt ttg gct gtg ggc atg cgg ccg 1104
124 Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro
125      355      360      365
127 gaa tgt gtg gtg ccc gaa aac cag tgt gca atg aaa cga cgc gaa aag 1152

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128	Glu	Cys	Val	Val	Pro	Glu	Asn	Gln	Cys	Ala	Met	Lys	Arg	Arg	Glu	Lys	
129		370					375					380					
131	aaa	gca	caa	aaa	gag	aag	gat	aaa	ata	cag	acc	agt	gtg	tgt	gca	acg	1200
132	Lys	Ala	Gln	Lys	Glu	Lys	Asp	Lys	Ile	Gln	Thr	Ser	Val	Cys	Ala	Thr	
133	385						390				395					400	
135	gaa	att	aaa	aag	gaa	ata	ctc	gat	tta	atg	aca	tgt	gaa	ccg	cca	tca	1248
136	Glu	Ile	Lys	Lys	Glu	Ile	Leu	Asp	Leu	Met	Thr	Cys	Glu	Pro	Pro	Ser	
137					405						410					415	
139	cat	cca	acg	tgt	ccg	ctg	tta	cct	gaa	gac	att	ttg	gct	aaa	tgt	caa	1296
140	His	Pro	Thr	Cys	Pro	Leu	Leu	Pro	Glu	Asp	Ile	Leu	Ala	Lys	Cys	Gln	
141				420						425				430			
143	gct	cgt	aat	ata	cct	cct	tta	tcg	tac	aat	caa	ttg	gca	gtt	ata	tat	1344
144	Ala	Arg	Asn	Ile	Pro	Pro	Leu	Ser	Tyr	Asn	Gln	Leu	Ala	Val	Ile	Tyr	
145			435					440					445				
147	aaa	tta	ata	tgg	tat	caa	gat	ggc	tac	gaa	cag	cca	tcc	gag	gaa	gat	1392
148	Lys	Leu	Ile	Trp	Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	
149		450					455					460					
151	ctc	aaa	cgt	ata	atg	agt	tca	ccc	gat	gaa	aat	gaa	agt	caa	cac	gat	1440
152	Leu	Lys	Arg	Ile	Met	Ser	Ser	Pro	Asp	Glu	Asn	Glu	Ser	Gln	His	Asp	
153	465					470					475					480	
155	gca	tca	ttt	cgt	cat	ata	aca	gaa	atc	act	ata	cta	aca	gta	caa	tta	1488
156	Ala	Ser	Phe	Arg	His	Ile	Thr	Glu	Ile	Thr	Ile	Leu	Thr	Val	Gln	Leu	
157					485					490					495		
159	att	gtg	gaa	ttt	gcc	aag	ggc	ttg	cca	gcg	ttt	acc	aaa	ata	cca	caa	1536
160	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	Thr	Lys	Ile	Pro	Gln	
161				500					505					510			
163	gag	gat	caa	ata	aca	cta	tta	aag	gcc	tgc	tca	tca	gaa	gtt	atg	atg	1584
164	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	
165			515					520					525				
167	ttg	cga	atg	gca	cga	cgt	tac	gat	cac	aat	tca	gat	tcg	ata	ttc	ttt	1632
168	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Asn	Ser	Asp	Ser	Ile	Phe	Phe	
169		530					535					540					
171	gcc	aat	aat	cga	tcg	tat	acg	cgt	gac	tct	tat	aaa	atg	gct	ggc	atg	1680
172	Ala	Asn	Asn	Arg	Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	Lys	Met	Ala	Gly	Met	
173	545					550				555						560	
175	gct	gat	aat	att	gag	gat	ctg	ctg	cat	ttc	tgt	cga	caa	atg	tac	tcg	1728
176	Ala	Asp	Asn	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Gln	Met	Tyr	Ser	
177					565					570					575		
179	atg	aaa	gtg	gac	aat	gtc	gaa	tat	gct	cta	ctc	act	gcc	att	gtg	atc	1776
180	Met	Lys	Val	Asp	Asn	Val	Glu	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	
181				580						585				590			
183	ttt	tcc	gat	cgg	ccg	ggc	ctc	gaa	gaa	gcc	gaa	cta	gtc	gaa	gcg	ata	1824
184	Phe	Ser	Asp	Arg	Pro	Gly	Leu	Glu	Glu	Ala	Glu	Leu	Val	Glu	Ala	Ile	
185			595				600						605				
187	caa	agt	tac	tac	atc	gat	aca	ctc	cgc	att	tac	ata	ctt	aat	cgc	cat	1872
188	Gln	Ser	Tyr	Tyr	Ile	Asp	Thr	Leu	Arg	Ile	Tyr	Ile	Leu	Asn	Arg	His	
189		610					615					620					
191	tgc	ggc	gat	ccc	atg	agt	ctc	gta	ttc	ttt	gcc	aag	ctt	ctg	tca	att	1920
192	Cys	Gly	Asp	Pro	Met	Ser	Leu	Val	Phe	Phe	Ala	Lys	Leu	Leu	Ser	Ile	

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193 625          630          635          640
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196 Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe
197          645          650          655
199 tcg ttg aaa ttg aaa aat cgc aaa ctg cca aaa ttc ctc gaa gag atc 2016
200 Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
201          660          665          670
203 tgg gat gta cat gcc att cca ccc tca gtg cag tca cac ata cag gct 2064
204 Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Ile Gln Ala
205          675          680          685
207 acc cag gcg gaa aag gcc gcc cag gaa gct cag gca aca aca tcg gcc 2112
208 Thr Gln Ala Glu Lys Ala Ala Gln Glu Ala Gln Ala Thr Thr Ser Ala
209          690          695          700
211 att tca gca gcc gcc acc tca tct tcc tcc ata aat acc tcg atg gca 2160
212 Ile Ser Ala Ala Ala Thr Ser Ser Ser Ser Ile Asn Thr Ser Met Ala
213 705          710          715          720
215 aca tca tcc tca tca tcg tta tcg cca tcg gcg gcc tca aca ccc aat 2208
216 Thr Ser Ser Ser Ser Ser Leu Ser Pro Ser Ala Ala Ser Thr Pro Asn
217          725          730          735
219 ggt ggt gcc gtc gat tat gtt ggc acc gat atg agt atg agt tta gta 2256
220 Gly Gly Ala Val Asp Tyr Val Gly Thr Asp Met Ser Met Ser Leu Val
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223 caa tcg gat aat gca tag 2274
224 Gln Ser Asp Asn Ala
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230 <212> TYPE: PRT
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238 20 25 30
240 Val Leu Ser Ser Asp Ile Asn Met Ser Pro Ser Ser Leu Asp Ser Pro
241 35 40 45
243 Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr
244 50 55 60
246 Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr
247 65 70 75 80
249 Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
250 85 90 95
252 Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn
253 100 105 110
255 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val
256 115 120 125
258 Gly Gly Gly Gly Gly Gly Gly Gly Val Pro Gly Met Thr Ser Leu Asn
259 130 135 140
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265						165				170					175	
267	Ser	His	His	Thr	Asn	Gly	His	Met	Gly	Ile	Gly	Gly	Gly	Gly	Gly	Gly
268				180					185					190		
270	Leu	Ser	Val	Asn	Ile	Asn	Gly	Pro	Asn	Ile	Val	Ser	Asn	Ala	Gln	Gln
271			195					200					205			
273	Leu	Asn	Ser	Leu	Gln	Ala	Ser	Gln	Asn	Gly	Gln	Val	Ile	His	Ala	Asn
274		210						215				220				
276	Ile	Gly	Ile	His	Ser	Ile	Ile	Ser	Asn	Gly	Leu	Asn	His	His	His	His
277	225					230					235					240
279	His	His	Met	Asn	Asn	Ser	Ser	Met	Met	His	His	Thr	Pro	Arg	Ser	Glu
280				245						250					255	
282	Ser	Ala	Asn	Ser	Ile	Ser	Ser	Gly	Arg	Asp	Asp	Leu	Ser	Pro	Ser	Ser
283				260					265					270		
285	Ser	Leu	Asn	Gly	Phe	Ser	Thr	Ser	Asp	Ala	Ser	Asp	Val	Lys	Lys	Ile
286			275					280					285			
288	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Leu	Gln	Glu	Glu	Leu	Cys	Leu	Val	Cys
289		290					295					300				
291	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Glu	Gly
292	305					310					315					320
294	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Thr	Lys	Asn	Ala	Val	Tyr	Cys
295					325					330					335	
297	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys
298				340					345					350		
300	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Ala	Val	Gly	Met	Arg	Pro
301		355						360					365			
303	Glu	Cys	Val	Val	Pro	Glu	Asn	Gln	Cys	Ala	Met	Lys	Arg	Arg	Glu	Lys
304		370					375					380				
306	Lys	Ala	Gln	Lys	Glu	Lys	Asp	Lys	Ile	Gln	Thr	Ser	Val	Cys	Ala	Thr
307	385					390					395					400
309	Glu	Ile	Lys	Lys	Glu	Ile	Leu	Asp	Leu	Met	Thr	Cys	Glu	Pro	Pro	Ser
310					405					410					415	
312	His	Pro	Thr	Cys	Pro	Leu	Leu	Pro	Glu	Asp	Ile	Leu	Ala	Lys	Cys	Gln
313				420					425					430		
315	Ala	Arg	Asn	Ile	Pro	Pro	Leu	Ser	Tyr	Asn	Gln	Leu	Ala	Val	Ile	Tyr
316			435					440					445			
318	Lys	Leu	Ile	Trp	Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp
319		450					455					460				
321	Leu	Lys	Arg	Ile	Met	Ser	Ser	Pro	Asp	Glu	Asn	Glu	Ser	Gln	His	Asp
322	465					470					475					480
324	Ala	Ser	Phe	Arg	His	Ile	Thr	Glu	Ile	Thr	Ile	Leu	Thr	Val	Gln	Leu
325					485					490					495	
327	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	Thr	Lys	Ile	Pro	Gln
328				500					505					510		
330	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met
331			515					520					525			
333	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Asn	Ser	Asp	Ser	Ile	Phe	Phe
334		530					535					540				

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 15,18

Seq#:28; N Pos. 19

VERIFICATION SUMMARY

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Input Set : A:\53-99a.app

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L:2164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0

L:2234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0